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Frequency and mutational patterns of multidrug resistance tuberculosis by MTBDRplus assay in Northern India

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Background: The worldwide increase in the emergence and spread of multidrug-resistant (MDR) tuberculosis (resistance to at least rifampin and isoniazid has made the timely identification of resistant *Mycobacterium tuberculosis* complex (MTBC) strains to achieve accurate and rapid diagnosis of drug resistant TB and an effective disease management and to prevent their spread is extremely important. The aim of this study was to investigate the frequency and patterns of mutations conferring resistance to MDR-TB isolates from tuberculosis patients in Northern India.

Methods: We performed an assessment of Geno Type® (HAIN Lifescience GmbH, Germany) on a total of twenty eight MDR-TB strains isolated from different patients at tertiary care hospital during Jan 2010-Dec 2011. This assay was designed to detect mutations within the 81-bp hot spot region of *rpoB*, *katG* codon 315, and mutations in the regulatory region of *inhA*.

Results: In 28 MDR-TB isolates, the most frequently mutated codons in *rpoB* gene were 16 (57.2%) S531L and 7(25%) D516V. S315T1 was noted in 26(92.8%) *katG* gene and C15T was present in 3(10.7%) *inhA* gene. Mutations in codon 531 of the rpoB gene and codon 315 of the katG gene dominated in RIF and INH resistant strains respectively ($p<0.05$). Mutational data showed that genetic changes in *rpoB, katG* and *inhA* gene were more consistently association with a significant resistance phenotype of MDR-TB.

Conclusion: MTBDRplus assay is a rapid and easy-to-perform test for the detection of the most common mutations found in MDR *M. tuberculosis* complex strains within one working day and can easily be included in routine work to diagnose drug resistance TB.

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Longitudinal molecular epidemiological study of multidrug resistant TB and transition to extensively drug resistance in eastern rual China

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Background: Continuous understanding of the epidemiology and evolution of multidrug resistant TB (MDR-TB) is key to develop the appropriate strategies for preventing its epidemic. The present study aimed to investigate the longitudinal trend of its rates, transmissions and transition to extensively drug resistant TB(XDR-TB), in an attempt to adjust the TB control activities in eastern rural China.

Methods: The data presented here span 8 years (2003-2010) and consisted of three population-based investigation of drug resistant TB in terms of socio-demographic and clinical characteristics of drug resistant TB cases as well as the microbiological and molecular features of their infected Mtb strains, respectively in one 19 years' DOTS covered eastern rural county: Deqing (DQ) and the other 9 years' DOTS covered Guanyun (GY).

Results: Within 9 years' study, 901 TB patients were identified at local TB dispensaries in two counties, with 254 resistant to at least one of 1st line drugs. Of the 135 MDR-TB isolates, 6 were XDR-TB. Rate of drug resistant TB remained stable, even reduced in some period both in two counties, while the rate of MDR-TB and MDR-TB plus resistance to fluoroquinolones increased significantly respectively from 14.5% and 5.1% in 2003/2004 to 21.3% and 9.7% in 2009/2010. The IS*6110* RFLP genotyping revealed the 21 clusters involving 48(28.4%) drug resistant TB cases in DQ and 28 clusters involving 59(32.1%) drug resistant TB cases in GY. The clustering proportion increased among the drug resistant TB cases especially for MDR-TB over the study period, reaching 52%(DQ) and 48%(GY) in 2010. And 2 XDR-TB isolates was identified within only 2 clusters 0f drug resistant Mtb in DQ. Designated as subtypes of Beijing family, totally 3 clusters (11 drug resistant TB cases) typical with katG315Thr mutation, persisted throughout the study period in two counties.

Conclusion: A high increased recent transmission of MDR-TB might implicate it necessary to improve the effectiveness on diagnosis and treatment of MDR-TB. Despite an increasing trend of MDR plus the resistant to fluoroquinolones, the low proportion of XDR-TB among MDR-TB might indicate it neccessary to cautiously introduce some of 2 line drugs in MDR-TB treatment in China.

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